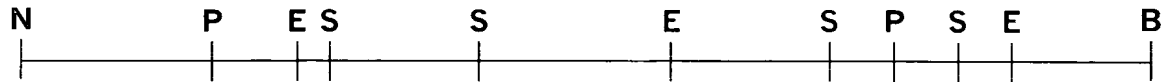


Figure 1: Restriction pattern of the HAL coding region cut with selected enzymes.

HAL



N - NdeI site introduced at the N-terminus

B - BamHI site introduced at the C-terminus

E - EagI

P - PstI

S - SphI

Figure 2: Experimentally derived peptide sequences of HAL

N-terminal

(M)ASAPQITLGLSGATAD

Internal

(M)ALADLDELLDEA

(M)GEPVEREVLRA

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Figure 3: SphI digestion pattern of HAL gene showing oligonucleotide and subclones.

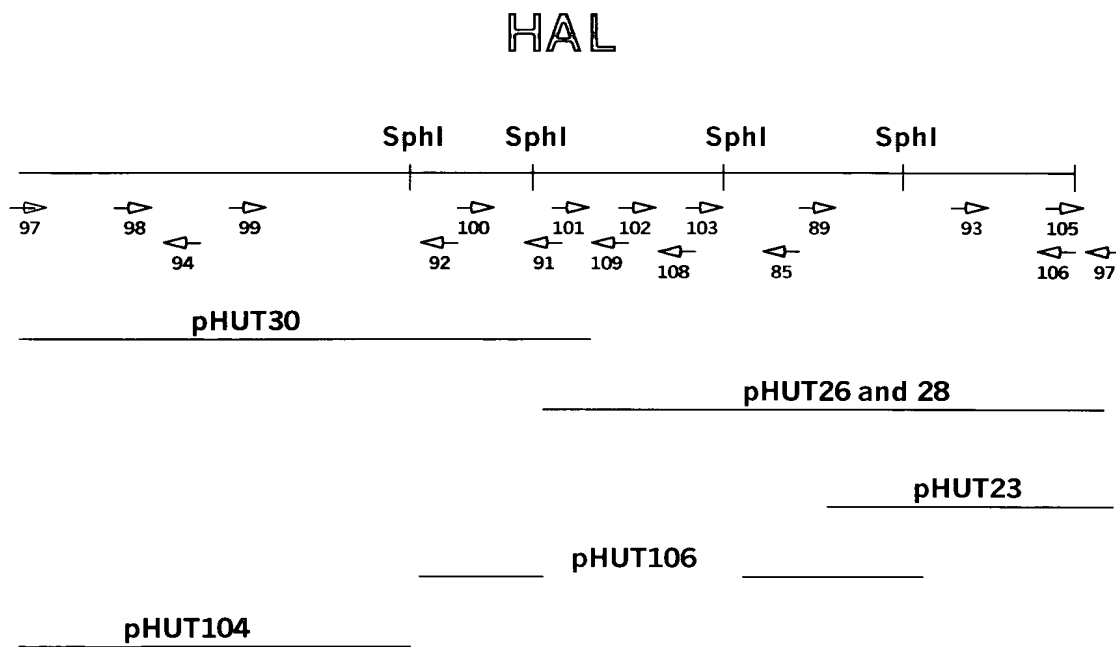
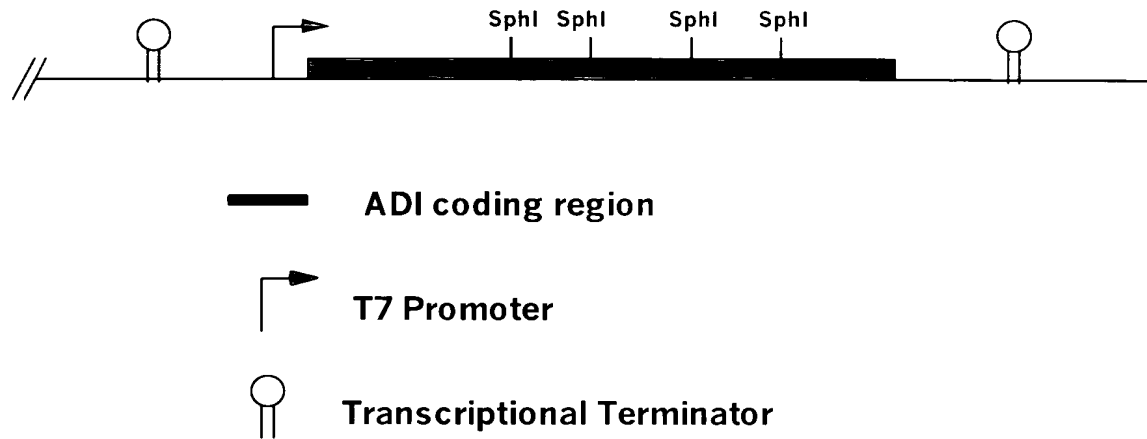


Figure 4: Histidine ammonia lyase overexpressing plasmid.

pHUT102



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Figure 5: SDS-PAGE showing expression of HAL in *E. coli*.

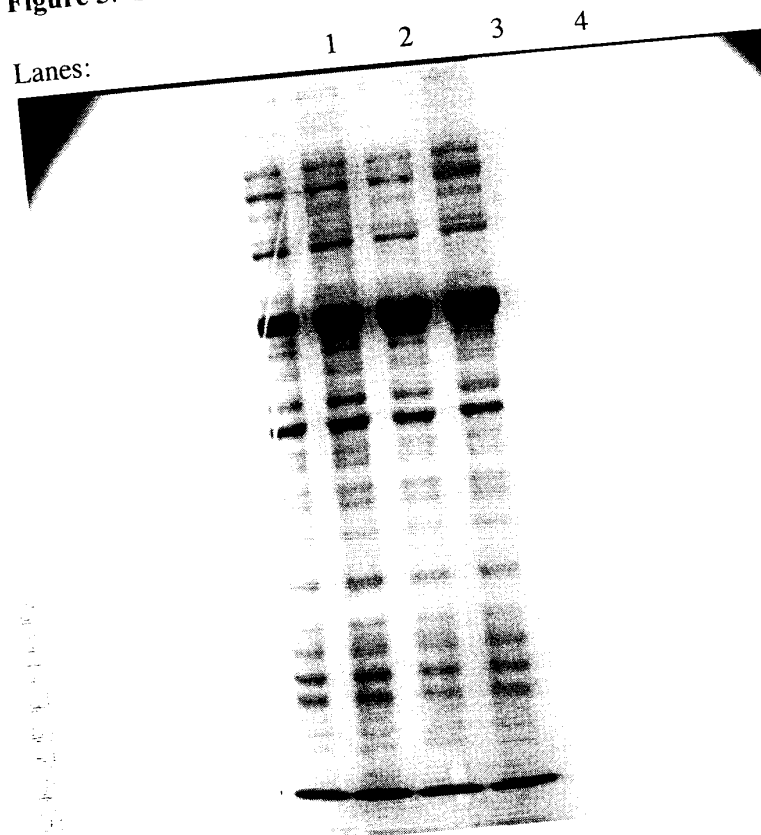
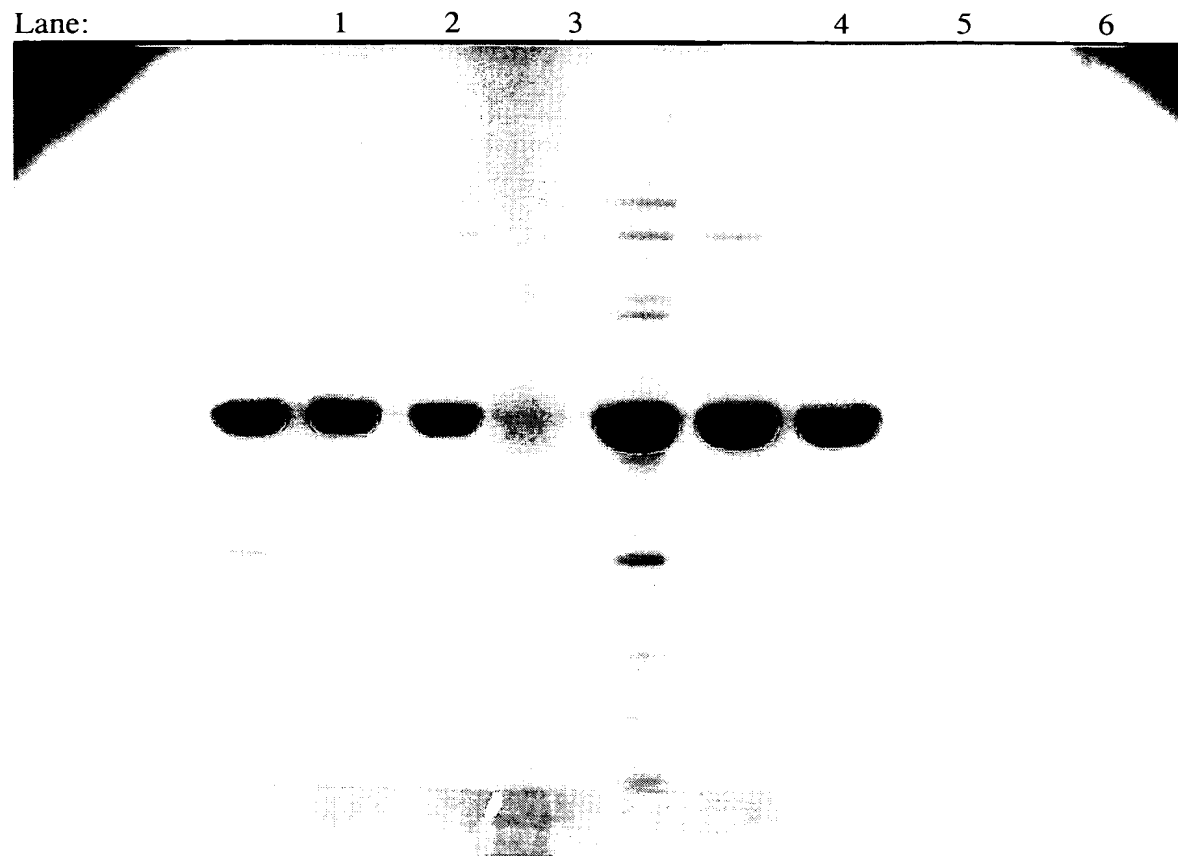
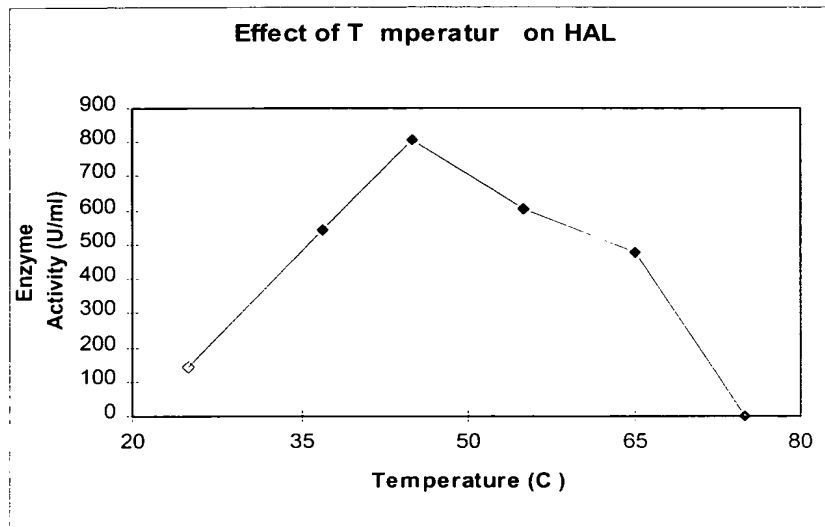


Figure 6: SDS-PAGE showing purification of HAL from *E. coli*



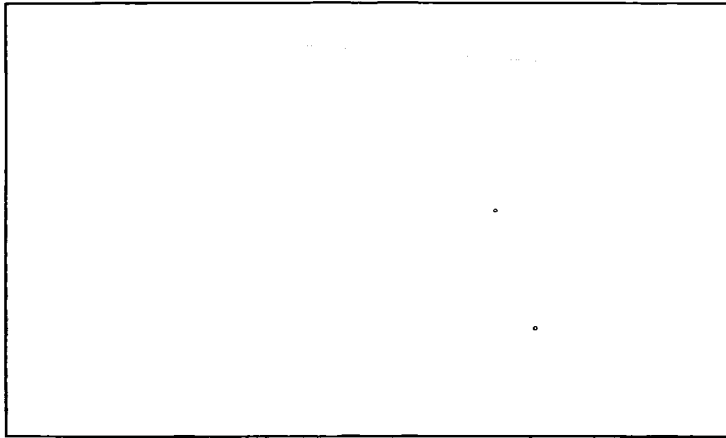
09833745-041201
FIG. 6

Figure 7: Effect of Temperature on HAL



078728/0106

Figure 8: Effect of pH on HAL.



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Figure 9: Effect of HAL and Histidinol on HSV.

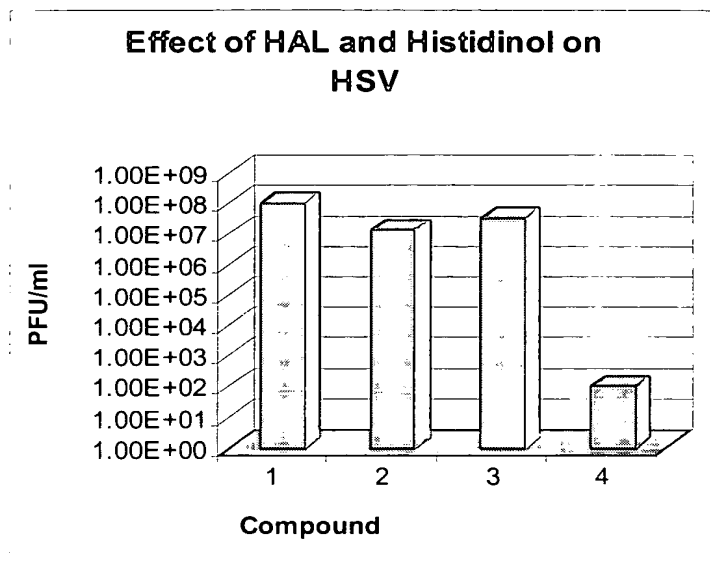
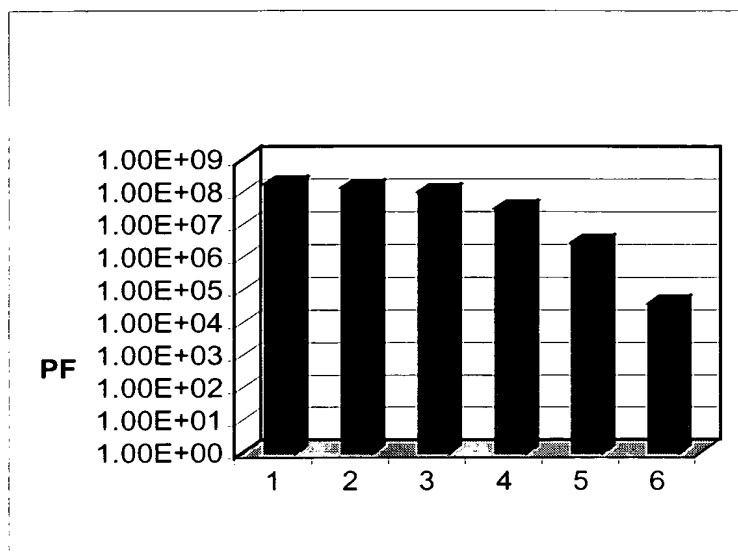


FIG. 9

Figure 10: Effectiveness of L-histidinol as a Single Agent



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Figure 11: Effect of HAL and Histidinol on RSV.

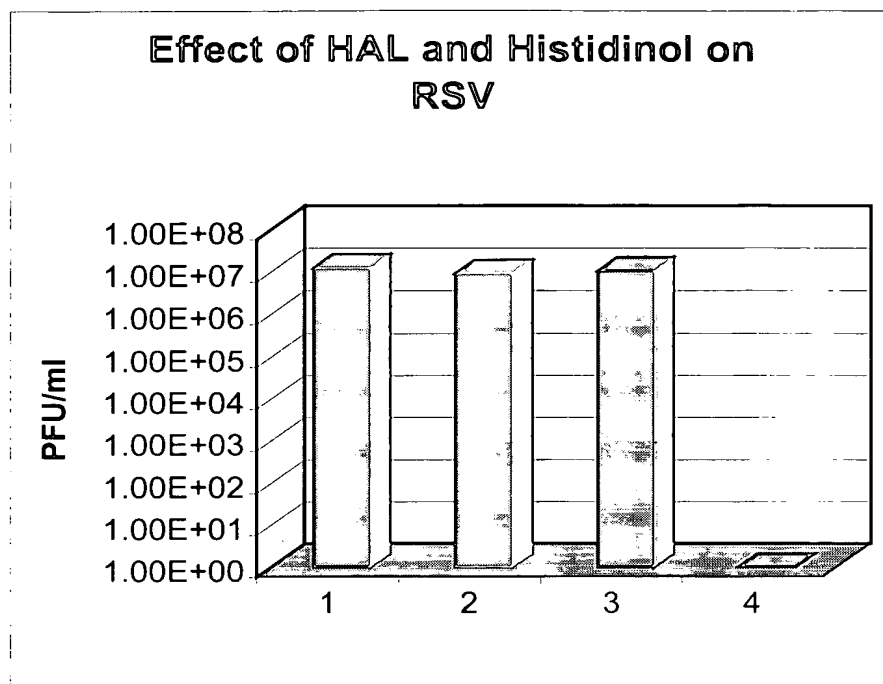


FIG. 11

DOCKET NO.: 078728/0106

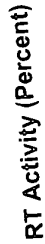
[illegible]

Figure 13: Histidine ammonia lyase peptide sequence pileup

HUTH_PSEPU -----
 -
 HUTH_RHIME -----
 -
 HUTH_MOUSE
 MPRYTVHVRGEWLAVPCQDGKLTVGWLGREAVRRYMKNKPDNGGFTSVDEVQFLVHRCKG
 HUTH_RAT
 MPRYTVHVRGEWLAVPCQDGKLSVGWLGREAVRRYMKNKPDNGGFTSVDEVRFVLRCKG
 HUTH_HUMAN
 MPRYTVHVRGEWLAVPCQDAQLTVGWLGREAVRRYIKNKPDNGGFTSVDDAHFLVRRCKG
 HUTH_CAEEL -MRLQVQIGTECVVVPCKP-DDTIHAVAKKSVEKLRRRLRPK----
 LPLADDYFEVRRTVG
 HUTH_BACS -----
 -
 HUTH_STRGR -----
 -
 HUTH_CORY -----
 -
 HUTH_PSEPU -----
 -
 HUTH_RHIME -----
 -
 HUTH_MOUSE LGLLDNEDELEVALEDNEFVEVVIEGDVMS-----PDFIPSQPEGVFLYSKYR---
 -
 HUTH_RAT LGLLDNEDLLEVALEDNEFVEVVIEGDVMS-----PDFIPSQPEGVFLYSKYR---
 -
 HUTH_HUMAN LGLLDNEDRLEVALENNEFVEVVIEGDAMS-----PDFIPSQPEGVYLYSKYR---
 -
 HUTH_CAEEL
 NSLLDPEDLVSDVLKDSDFIIVAASVEETEDAKEAKKQEEIDNARAEIEKIDNRRRKVSF
 HUTH_BACS -----
 -
 HUTH_STRGR -----
 -
 HUTH_CORY -----
 -
 HUTH_PSEPU -----
 TELTLKPGTLTLAQLRAIHAAPVRLQLDASAAPIDASVACVEQIIA
 HUTH_RHIME -----
 MTVILRPGSVPLSDLETIYWTGAPARLDAAFDAGIAKAAARIAEIVA
 HUTH_MOUSE -----
 EPEKYIALDGDSLSTEDLVNLGKGGRYKIKLTSIAEKKVQQSREVIDSIK
 HUTH_RAT -----
 EPEKYIALDGDSLSTEDLVNLGKGGRYKIKLTSIAEKKVQQSREVIDSIK
 HUTH_HUMAN -----
 EPEKYIELDGDRLTEDLVNLGKGGRYKIKLTPAEKRVQKSREVIDSIK
 HUTH_CAEEL
 ADSLAPMVLAPPTKLLILDGNSLLPEDLVRCEKGECAIQLSMESEDRIRKARTFLEKIAS
 HUTH_BACS -----
 MVTLDGSSLTTADVAVRLFDFEEAAASEESMERVKKSRAAVERIVR
 HUTH_STRGR -----
 MDMHTVVVGTSGTTAEDVVAVARHGARVELSAAAVEALAAARLIVDALAA
 HUTH_CORY -----
 MASAPQITLGLSGATADDVIAVARHEARISISPQVLEELASVRAHIDALAS

Figure 13 cont'd.

HUTH_PSEPU
EDRTAYGINTGFGLLASTRIASHDLENLQSLVLSHAAGIGAPLDDDLVRLIMVLKINSL
HUTH_RHIME
GNAPVYGINTGFGKLASIKIDSSDVATLQNLILSHCCGVGQPLTEDIVRLIMALKLISL
HUTH_MOUSE
ERTVVYGITTGFGKFARTVIPANKLQELQVNLVRSHSSGVGKPLSPERCRLMLLALRINVL
HUTH_RAT
ERTVVYGITTGFGKFARTVIPANKLQELQVNLVRSHSSGVGKPLSPERCRLMLLALRINVL
HUTH_HUMAN
EKTVVYGITTGFGKFARTVIPINKLQELQVNLVRSHSSGVGKPLSPERCRLMLLALRINVL
HUTH_CAEEL
EHRAVYGVTGFGTFSNVTIPPEKLKKLQNLIRSHATGYGEPLAPNRARMLLALRINIL
HUTH_BACS
DEKTIYGINTGFGKFSVDLIQKEDSAALQNLILSHACGVGDFFPECVSRAMLLLRANAL
HUTH_STRGR
KPEPVYGVSTGFGALASRHIGTELRAQLQRNIVRSHAAGMGPVEREVVRALMFLRLKTV
HUTH_CORY
ADTPVYGISTGFGALATRHIAPEDRAKLQSLIRSHAAGMGPVEREVVRALMFLRAKTL

0963745-041304
HUTH_PSEPU
SRGFSGIRRKVIDALIALVNAEVYPHPLKGSVGASGDLAPLATMSLVLLGEGKARYKGQ
HUTH_RHIME
GRGASGVRLLELVRLIEAMLDKGVIPLIPEKGSVGASGDLAPLAHMAAVMMGHGEAFFAGE
HUTH_MOUSE
AKGYSGISLETLKQVIEAFNASCLSYVPEKGTVGASGDLAPLSHLALGLIGEGKMWSPKS
HUTH_RAT
AKGYSGISLETLKQVIEFNASCLSYVPEKGTVGASGDLAPLSHLALGLIGEGKMWSPKS
HUTH_HUMAN
AKGYSGISLETLKQVIEMFNASCLPYVPEKGTVGASGDLAPLSHLALGLVGEKMWSPKS
HUTH_CAEEL
AKGHSGISVENIKKMIAAFNAFCVSYVPQQGTVGCSGDLCPHLALGLLGEKMWSPPT
HUTH_BACS
LKGFSGVRAELIEQLLAFLNKRVPVPIQQGSLGASGDLAPLSHLALALIGQGEVFFEGE
HUTH_STRGR
ASGHTGVRPEVAQTMADVNLNAGITPVVHEYGLCSGDLAPLSHCALTLMGEGEAEAGPDG
HUTH_CORY ASGRS-
VRPVVLETMVGMLNAGITPVVREYGLCSGDLAPLSHCALVLMGEGEATDAHG

HUTH_PSEPU -
WLSATEALAVAGLEPLTLAAKEGLALLNGTQASTAYALRGLFYAEDLYAAAIACGGLSV
HUTH_RHIME -
RMKGDAALKAAGLSPVTLAAKEGLALINGTQVSTALALAGLFRAHRAGQAALITGALST
HUTH_MOUSE
GWADAKYVLEAHGLKPIVLKPKEGLALINGTQMITSLGCEALERASAIARQADIVAALT
HUTH_RAT
GWADAKYVLEAHGLKPIVLKPKEGLALINGTQMITSLGCEAVERASAIARQADIVAALT
HUTH_HUMAN
GWADAKYVLEAHGLKPIVLKPKEGLALINGTQMITSLGCEAVERASAIARQADIVAALT
HUTH_CAEEL
GWQPADVVLKKNLEPLELGPKEGLALINGTQMVTALGAYTLERAHNIARQADVIAALS
HUTH_BACS -
RMPAMTGLKKAGIQPVTLTSKEGLALINGTQAMTAMGVVAYIEAEKLAYQTERIASLTI
HUTH_STRGR
TVRPAGELLAAHGIAPVELREKEGLALLNGTDGMLGMLVMAADLRNLYTSADITAALS
HUTH_CORY
DIRPVPELFAEAGLTPVELAEKEGLALVNGTDGMLGQLIMALADLDELDDIADATAAMSV

HUTH_PSEPU	EAVLGSRSPFDARIHE-ARGQRGQIDTAACFRDLLGDSSEVSLSHKNCD----
KVQDPYS	
HUTH_RHIME	DAAMGSSAPFHPDIQH-CAAIRARSTRAAALRQLLTG-SPIRQSHIEGDE---
RVQDPYC	
HUTH_MOUSE	EVLKGTTKAFDTDIHA-VRPHRGQIEVAFRFRSLLDS-
DHHPSEIAESHRFCDRVQDAYT	
HUTH_RAT	EVLKGTTKAFDTDIHA-VRPHRGQIEVAFRFRSLLDS-
DHHPSEIAESHRFCDRVQDAYT	
HUTH_HUMAN	EVLKGTTKAFDTDIHA-LRPHRGQIEVAFRFRSLLDS-
DHHPSEIAESHRFCDRVQDAYT	
HUTH_CAEEL	DVLKGTTRAYDPDIHR-IRPHRGQNL SALRLRALLHS-
EANPSQIAESHRNCTKVQDAYT	
HUTH_BACS	EGLQGIIDAFDEDIHL-ARGYQEQIDVAERIRFYLSD-SGLTTSQGE-----
LRVQDAYS	
HUTH_STRGR	EALLGTDKVLAPELHA-IRPHPGQGV SADNMSRVLAG-SGLTGHHQDDAP---
RVQDAYS	
HUTH_CORY	EAQLGTDQVFRAELHEPLRPHPGQGRSAQNMF AFLAD-SPIVASHREGDG---
RVQDAYS	

HUTH_PSEPU ALATAIEIGSLSEIRISLMDKHMS-
QLPPFLVENGGVNSGFMIQVTTAAALASENKALSH
HUTH_RHIME
ALAVCEIGAISQRRIALLVDPALSLRLPAFLAKKPGLSGLMIAEVTSAALMSENKQLSH
HUTH_MOUSE AIGVHELAAISERRIERLCNPSSL-
ELPAFLVAEGGLNSGFMIHCTAAALVSESKALCH
HUTH_RAT AIGVHELAAISERRIERLCNPSSL-
ELPAFLVAEGGLNSGFMIHCTAAALVSESKALCH
HUTH_HUMAN AIGIHELAAISERRIERLCNPSSL-
ELPAFLVAEGGLNSGFMIHCTAAALVSENKALCH
HUTH_CAEEL AIAVAELAQMSERRLERLVNKELS-
GLPTFLTLPDGGLSNGFMTVQLCAASLVSENKVLCH
HUTH_BACS KIAISELANIAERRIERLVNPQLN-
DLPPFLSPHPGLQSGAMIMQYAAASLVSENKTLAH
HUTH_STRGR
AIVAADLGSICERRTDRLLDKNRSHGLPPFLADDAGVDSGLMIAQYTQAALVSEMKRLAV
HUTH_CORY
AIAVADLGSIAERRTDRMLDPAERSRDLPAFLADDPGVDSGMMIAQYTQAGLVAENKRLAV

Figure 13 cont'd.

HUTH_PSEPU	PHSVDSLPTSANQEDHVSMAPAAGKRLWEMAENTRGVPAIEWLGACQGLDLRKG-LKTS
HUTH_RHIME	PASVDSTPTSANQEDHVSMACHGARRLLQMTENLFSIIGIEALAAVQGIEFRAP-LTTS
HUTH_MOUSE	PSSVDSLSTSAATEDHVSMGGWAARKALRVVEHVEQVLAIELLAACQGIEFLRP-LKTT
HUTH_RAT	PSSVDSLSTSAATEDHVSMGGWAARKALRVIEHVEQVLAIELLAACQGIEFLRP-LKTT
HUTH_HUMAN	PSSVDSLSTSAATEDHVSMGGWAARKALRVIEHVEQVLAIELLAACQGIEFLRP-LKTT
HUTH_CAEEL	PSSVDSIPTSCNQEDHVSMGGFAARKALTVVEHVEAVLAMELLAACQGIEFLKP-LIST
HUTH_BACS	PASVDSIPSSANQEDHVSMGTIAARHAYQVIANTRRVIAIEAICALQAVEYRGI-EHAA
HUTH_STRGR	
PASADSIPSSAMQEDHVSMGWSAARKLRTAVDNLARIVAVELYAATRAIELRAAEGLTPA	
HUTH_CORY	PA-VDSIPSSAMQEDHVSLGWHAARKLPTSVANLRRILAVEMLIAGRALDLRAP-LKPG
HUTH_PSEPU	AKLEKARQALRSEVA-HYDRDRFFAPDIEKAVELLAKG---S-LTGLLPAGVLPSSL---
-	
HUTH_RHIME	PELQKAAAARVGVSS-SIEEDRYMADDLKAAGDLVASG---R-LAAAVSAGILPKLEN-
HUTH_MOUSE	TPLEKVYDLVRSVVR-
PWIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEKYRMEHIPESR	
HUTH_RAT	TPLEKVYDLVRSVVR-
PWIKDRFMAPDIEAAHRLLLDQKVWEVAAPYIEKYRMEHIPESR	
HUTH_HUMAN	TPLEKVYDLVRSVVR-
PWIKDRFMAPDIEAAHRLLEQKVWEVAAPYIEKYRMEHIPESR	
HUTH_CAEEL	APLHKIYQLVRSVAP-
PLNEDRYMKPEIDAVLEMIRENRIWEAVLPHLETLEAMEELDPD	
HUTH_BACS	SYTKQLFQEMRKVVP-SIQQDRVFSYDIERLTDWLKK----ESLIPDHQNKELRGMNI-
HUTH_STRGR	PASEAVVAALRAAGAEGPGPDRFLAPDLAAADTFVREG---R-LVAAVEPVTGPLA---
-	
HUTH_CORY	PATGAVLEVLRSKVA-GPGQDRFLSAELEAAYDLLANG---S-VHKALEAHLPE-----
-	
HUTH_PSEPU	-----
HUTH_RHIME	-----
HUTH_MOUSE	PLSPTAFSLES LRKNSATIPESDDL----
HUTH_RAT	PLSPTAFSLES LRKNSATIPESDDL----
HUTH_HUMAN	PLSPTAFSLQFLHKKSTKIPESEDL----
HUTH_CAEEL	ALRQFTKTPTGIVQDRSMIPISDDEESIE
HUTH_BACS	-----
HUTH_STRGR	-----
HUTH_CORY	-----

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Figure 14

	983831	1	80
1	SWALL: CAC21618	100.0%	MASAPQITLGLSGATADDVAVARHEARISISPOVLEEIASVRAHIDALASADTPVYGISTGFGALATRHIAPEADRAKLQ
2	SWALL: HUTH_STRGR	66.1%	---MHTVVVGTSVTASDVAVARAGARIELSEAEVAALAAARSVVDAALAAAPDPVYGVSTGFGALATRHISPELRGLQ
3	SWALL: HUTH_DEIRA	65.4%	-MDMHTVVVGTSVTAEADVAVARHARGARVELSAAAEALAAARLIVDALAAKPEPVYGVSTGFGALASRHIGTELRAQLQ
4	SWALL: BAB16159	46.8%	-----MILDRDLNLEQFISVVRHGQVELSAAARERARARTVIEQIVEGDTPIYGVNTGFGKFENVQIDRSQLAQLQ
5	SWALL: Q9KWE4	42.0%	-----VPLHHLADIYNNNGSAKLDPFSDAAVLKGAARAEIAAGNAPVYGVNTGFGKLASIKIDAADLALTLQ
6	SWALL: HUTH_BACSU	42.0%	-----VPLHHLADIYNNNGSAKLDPFSDAAVLKGAARAEIAAGNAPVYGVNTGFGKLASIKIDAADLALTLQ
7	SWALL: Q9KSQ4	40.4%	---MVLHLMIKPGQISLKLQROVSRSPVLSLDPDAIPATAESAQVVEQVISEGRTVYGVNTGFGKLANTKIAPODLETLQ
8	SWALL: Q9HU085	42.2%	---MSLHLKPGQTLADLRQAYLAPVRLSLDPSADAPTAASVACVENIIAEGRTAYGVNTGFGLLASTRISPADLEKLQ
9	SWALL: Q9KBE6	41.7%	--MTNLKLLDGRSLSLHDLHRIIYEGETVGSDESMEKVKQSRKAVEQIIVADEKIIYGVNTGFGKFSDFIDPDDVENLQ
10	SWALL: HUTH_PSEPU	39.3%	---TELTKPGTLTLAQLRAIHAAPVRLQLDASAAPDAIDASVACVEQIIAEDRTAYGVNTGFGLLASTRIASHDLENLQ
11	SWALL: HUTH_RHIME	41.7%	-----LRPGSVPLSDLETIYWTGAPARLDAAFDAGIAKAAARAEIIVAGNAPVYGVNTGFGKLASIKIDSDDVATLQ
12	SWALL: Q9HU090	40.6%	MSDLPSVVFGDGPRLRWQELVAVARHARGARLELSAAAWARIDNARAIVCRIVANGERAYGISTGLGALCDVLLGEQEALQS
13	SWALL: HUTH_HUMAN	40.7%	KYREPEKYIELDGLTTEDLVNLGKGRYKIKLTPTAEKRVQKSREVIDSIIKEKTVVYGVNTGFGKFA-RTVIPINKLQLQ
14	SWALL: HUTH_CAEEL	39.2%	VLAPPTKLLILDGNSPEDLVRCCKGECALQSMESDRIRKARTFLEKIASEHRAVYGVNTGFGTFSNVTIPEKLLKQLQ
15	SWALL: Q9HLI6	38.8%	-----MIEIDGRSLRVEDVYAVAVEYDRVSISSDRTLKAVEEKHEATKLINSKGTVYGVNTGFGSLINVHIERDQEIQLQ
16	SWALL: HUTH_MOUSE	41.0%	KYREPEKYIALDGDSTEDLVNLGKGRYKIKLTSIAEKKVQQSREVIDSIIKERTVVYGVNTGFGKFA-RTVIPANKLQLQ
17	SWALL: BAB29407	38.6%	KYREPEKYIALDGDSTEDLVNLGKGRYKIKLTSIAEKKVQQSREVIDSIIKERTVVYGVNTGFGKFA-RTVIPANKLQLQ
18	SWALL: HUTH_RAT	38.2%	KYREPEKYIALDGDSTEDLVNLGKGRYKIKLTSIAEKKVQQSREVIDSIIKERTVVYGVNTGFGKFA-RTVIPANKLQLQ
19	SWALL: AAG53586	39.8%	---MNALTLPGLTLTQAQLRQVWQQPLQTLTDESAHEAINDSVACVEAIVAEGRRTAYGVNTGFGLLAQTRATHDLENLQ
20	SWALL: Q9KKE0	38.9%	-----MGEMISLDGPLETWREIASIAEGASLDLSGPARLRITAAQARRIVDALVERGIRGYGVNTGVGALCDVIIISRENQQAQS
21	SWALL: Q9HQD5	42.2%	-----MSDTRIDAADREALQ

Figure 14, cont'd.

	983831	100.0%	81		1	160
1	SWALL: CAC21618	66.1%		RS	LIRSHAAAGMGE	PVEREVVRALMFLRAKTLASCR
2	SWALL: HUTH_STRGR	65.4%		RV	NRSHAAAGMGP	RVREVRALMFLRKTCVSGRTGVR
3	SWALL: HUTH_DEIRA	46.8%		RV	NRSHAAAGMGP	RVREVRALMFLRKTCVSGRTGVR
4	SWALL: BAB16159	42.0%		RV	NRSHAAAGMGP	RVREVRALMFLRKTCVSGRTGVR
5	SWALL: Q9KWE4	42.0%		RV	NRSHAAAGMGP	RVREVRALMFLRKTCVSGRTGVR
6	SWALL: HUTH_BACSU	40.4%		RV	NRSHAAAGMGP	RVREVRALMFLRKTCVSGRTGVR
7	SWALL: Q9KSQ4	42.2%		RV	NRSHAAAGMGP	RVREVRALMFLRKTCVSGRTGVR
8	SWALL: Q9HU85	41.7%		RV	NRSHAAAGMGP	RVREVRALMFLRKTCVSGRTGVR
9	SWALL: Q9KBE6	39.3%		RV	NRSHAAAGMGP	RVREVRALMFLRKTCVSGRTGVR
10	SWALL: HUTH_PSEPU	41.7%		RV	NRSHAAAGMGP	RVREVRALMFLRKTCVSGRTGVR
11	SWALL: HUTH_RHIME	40.6%		RV	NRSHAAAGMGP	RVREVRALMFLRKTCVSGRTGVR
12	SWALL: Q9HU90	40.7%		RV	NRSHAAAGMGP	RVREVRALMFLRKTCVSGRTGVR
13	SWALL: HUTH_HUMAN	39.2%		RV	NRSHAAAGMGP	RVREVRALMFLRKTCVSGRTGVR
14	SWALL: HUTH_CAEEL	38.8%		RV	NRSHAAAGMGP	RVREVRALMFLRKTCVSGRTGVR
15	SWALL: Q9HLI6	41.0%		RV	NRSHAAAGMGP	RVREVRALMFLRKTCVSGRTGVR
16	SWALL: HUTH_MOUSE	38.6%		RV	NRSHAAAGMGP	RVREVRALMFLRKTCVSGRTGVR
17	SWALL: BAB29407	38.6%		RV	NRSHAAAGMGP	RVREVRALMFLRKTCVSGRTGVR
18	SWALL: HUTH_RAT	38.2%		RV	NRSHAAAGMGP	RVREVRALMFLRKTCVSGRTGVR
19	SWALL: AAC53586	39.8%		RV	NRSHAAAGMGP	RVREVRALMFLRKTCVSGRTGVR
20	SWALL: Q9KKE0	38.9%		RV	NRSHAAAGMGP	RVREVRALMFLRKTCVSGRTGVR
21	SWALL: Q9HQD5	42.2%		RV	NRSHAAAGMGP	RVREVRALMFLRKTCVSGRTGVR

[illegible]

Figure 14, cont'd.

[illegible]

DETD" 3422660

Figure 14, cont'd.

	983831	321	400
1	SWALL: CAC21618	100.0%	VVLPSEVTSNGNFHGPVAYVLDFLAIVADLGSIAERTTRDMLDPARSRLDPAFLADDPGVDSGMMIAQYTOAGLVAE
2	SWALL: HUTH_STRGR	66.1%	VLPDGRVESNGNFHGPVAYVLDFLAIVADLGSIAERTTRDMLDKNRSHGLPPLADDDAGVDSGLMIAQYTOAALVGE
3	SWALL: HUTH_DEIRA	65.4%	VLPDGRVESNGNFHGPVAYVLDFLAIVADLGSIAERTTRDMLDKNRSHGLPPLADDDAGVDSGLMIAQYTOAALVSE
4	SWALL: BAB16159	46.8%	LIIFTGEVSVSGNFHGOPLAVTIDALKVAVALGSGISERRTEQLNPLS-GLPAFLTPNGGINSGLMIAQYTSAAALVSE
5	SWALL: Q9KWE4	42.0%	LVLSDNSVSGNFHGAEPVAFADQDTALAVCEIGATAQRRIALLVDPALSYGLPAFLSKKPGINSGLMIAEVTSAALMSE
6	SWALL: HUTH_BACSU	42.0%	LVLSDNSVSGNFHGAEPVAFADQDTALAVCEIGATAQRRIALLVDPALSYGLPAFLSKKPGINSGLMIAEVTSAALMSE
7	SWALL: Q9KSQ4	40.4%	LIFNDGDVVISGNGFHGOPIAFAMDFLKIAISELANIAERRIERLVNPN-QLN-DLPPFLSPHPGLQSGAMIMQYAAASLVSE
8	SWALL: Q9HU85	42.2%	LVFADGDIISGNGFHGAEPVAMAADNLALAEIGSLSERRMALLIDSALSK-LPPFLVDNGGVNSGFMIAQVTAALASE
9	SWALL: Q9KBE6	41.7%	LVFAAGDVISGNGFHGAEPVAMAADNLALAEIGSLSERRMALLIDSALSK-LPPFLVDNGGVNSGFMIAQVTAALASE
10	SWALL: HUTH_PSEPU	39.3%	LIFONGQVVISGNGFHGOPIAFAMDFLKIAISELANIAERRIERLVNPN-QLN-DLPPFLSAAPGVQSGVMILQYCAASLVSE
11	SWALL: HUTH_RHIME	41.7%	LVFAAGDVISGNGFHGAEPVAMAADNLALAEIGSLSERRMALLIDSALSK-LPPFLVDNGGVNSGFMIAQVTAALASE
12	SWALL: Q9HU90	40.6%	LVLSDNSVSGNFHGAEPVAFADQDTALAVCEIGATAQRRIALLVDPALSYGLPAFLSKKPGINSGLMIAEVTSAALMSE
13	SWALL: HUTH_HUMAN	40.7%	LLLTGTPVVSQANPHGESVMAADLLAIAVAELGVAERRLDRLVNPVLS-GLPAFLVGKPGVNSGMMITQYVAASLAGE
14	SWALL: HUTH_CAEEL	39.2%	MVFANGETVSGNGFHGEYPAKALDYLAIGIHELAASERRIERLCNPSLS-ELPAFLVAEGGINSGFMAHCTAAALVSE
15	SWALL: Q9HLI6	38.8%	LVFADREIISGNGFHGEYPAKALDYLAIGIHELAASERRIERLCNPSLS-ELPAFLVAEGGINSGFMAHCTAAALVSE
16	SWALL: HUTH_MOUSE	41.0%	L-FNGEEVSVSGNFHGEYPAKALDYLAIGIHELAASERRIERLCNPSLS-ELPAFLVAEGGINSGFMAHCTAAALVSE
17	SWALL: BAB29407	38.6%	MVFASGETISGNGFHGEYPAKALDYLAIGIHELAASERRIERLCNPSLS-ELPAFLVAEGGINSGFMAHCTAAALVSE
18	SWALL: HUTH_RAT	38.6%	MVFASGETISGNGFHGEYPAKALDYLAIGIHELAASERRIERLCNPSLS-ELPAFLVAEGGINSGFMAHCTAAALVSE
19	SWALL: AAG53586	38.2%	LVFAANEMVFRGNGFHGAEPVAMAADNLALAEIGALSERRIALMMDKHSQ-LPPFLVRNGGVNSGFMIAQVTAALASE
20	SWALL: Q9KKE0	39.8%	AVAGSPEVHQAHAVALGLAMDLSAVAEEVAALSERRIDRLVNPVLS-GLPAFLAGDSGVSSGFMIAQVTAALASE
21	SWALL: Q9HQD5	38.9%	LVFPSTGVVSGNFHGEVLAURLGYAASALAEALASERRTRDRLNPNETQEPLEPFLAPDSGLHSLMIPQYTAASLVND
		42.2%	

Sequence

Figure 14, cont'd.

983831	481	100.0%	[5] 513
1	SWALL: CAC21618	66.1%	PGQDRFLSAELEAAAYDLLANGSVHKALEAHLPA		
2	SWALL: HUTH_STRGR	65.4%	PGPDRHLAPDLAAADAFVRAGHIVAAAE SVTGP		
3	SWALL: HUTH_DEIRA	46.8%	PGPDRFLAPDLAAADTFVREGRLVAAVEPVTGP		
4	SWALL: BAB16159	42.0%	LTEDRYFRPDLRLRGELVSGRVAQAADTQAPA		
5	SWALL: Q9KWE4	42.0%	LEDDRYMATDLKAAIEVVASGALVSAISSGLPV		
6	SWALL: HUTH_BACSU	40.4%	LEDDRYMATDLKAAIEVVASGALVSAISSGLPV		
7	SWALL: Q9KSQ4	42.2%	IQQDRVFSYDIERTDMLKKESLIPDHQNKELR		
8	SWALL: Q9HU85	41.7%	YKD RYFAPDIEKANALL-QLAVHNRLMPDQLL		
9	SWALL: Q9KBE6	39.3%	YQEDRFFAPDIEAASQLLASGCLNALLPARLLP		
10	SWALL: HUTH_PSEPU	41.7%	IDODRMFAKDIERAAKWLKDGSDFTKMKREKER		
11	SWALL: HUTH_RHIME	40.6%	YDRDRFFAPDIEKAVELLAKGSLTGLLPAGLPS		
12	SWALL: Q9HU90	40.7%	IEEDRYMADDLKAAGDLVASGRLAASVAGLPG		
13	SWALL: HUTH_HUMAN	39.2%	YDTRWLAPDIAAAILGERKSLARLAASIGD		
14	SWALL: HUTH_CAEEL	38.8%	WIKDRFMADIEAAHRLLEQKVWEVAAPIYIEK		
15	SWALL: Q9HLI6	41.0%	PNEDRYMKPEIDAVLEMIRENRIWEAVLPHLET		
16	SWALL: HUTH_MOUSE	38.6%	LDHDRPPSFEDIETIRKMDKKEFISALP-----		
17	SWALL: BAB29407	38.6%	WIKDRFMADIEAAHRLLEQKVWEVAAPIYIEK		
18	SWALL: HUTH_RAT	38.2%	WIKDRFMADIEAAHRLLEQKVWEVAAPIYIEK		
19	SWALL: AAGS3586	39.8%	YDDDRFFAPDIEAAISLLNKGSLVGLLPAPFL--		
20	SWALL: Q9KKE0	38.9%	PIATIVR-----		
21	SWALL: Q9HQD5	42.2%	PAGDRALADDDMAAVGDLVRAGLVEDAVARALDA		

TOE T H O " S T R E E B E A

Figure 14, cont'd.

KEY:

983831 : HAL

1	CAC21618	: Streptomyces coelicolor
2	HUTH_STRGR	: Streptomyces griseus
3	HUTH_DEIRA	: Deinococcus radiodurans
4	BAB16159	: Agrobacterium rhizogenes
5	Q9KWE4	: Agrobacterium rhizogenes
6	HUTH_BACSU	: Bacillus subtilis
7	Q9KSQ4	: Vibrio cholerae
8	Q9HU85	: Pseudomonas aeruginosa
9	Q9KBE6	: Bacillus halodurans
10	HUTH_PSEPU	: Pseudomonas putida
11	HUTH_RHIME	: Rhizobium meliloti
12	Q9HU90	: Pseudomonas aeruginosa
13	HUTH_HUMAN	: Human
14	HUTH_CAEEL	: Caenorhabditis elegans
15	Q9HLI6	: Thermoplasma acidophilum
16	HUTH_MOUSE	: Mouse
17	BAB29407	: Mus musculus (Mouse)
18	HUTH_RAT	: Rat
18	AAG53586	: uncultured bacterium pCosAS1
20	Q9KKE0	: Rhizobium meliloti
21	Q9HQD5	: Halobacterium sp

FIG. 15

Figure 15

STRG	6	VVVGTSGTTAEDVAVARHGARVELSAAAVEALAAARLIVDALAAKPEPVYGVSTGFGAL	
"HAL"	7	ITLGLSGATADDVIAVARHEARISISPOVLEELASVRAHIDALASADTPVYGISTGFGAL	
		* * * * *	* * * * *
		* * * * *	* * * * *
STRG,	66	ASRHIGTELRAQLQRNIVRSHAAGMGRVEREVVRALMFLRLKTVASGHTGVRPEVAQTM	
HAL	67	ATHRIAPEDRAKLQRLIRSHAAGMGPVEREVVRALMFLRAKTLASGRTGVRPVVLETM	
		* * * * *	* * * * *
		* * * * *	* * * * *
STRG	126	ADVLNAGITPVVHEYGSLGCSGDLAPLSHCALTLMGEAGEGPDGTVRPAGELLAAHGIA	
HAL	127	VGMLNAGITPVVREYGSLGCSGDLAPLSHCALVLMGEGEATDAHGDIRPVPPELFAEAGLT	
		* * * * *	* * * * *
		* * * * *	* * * * *
STRG	186	PVELREKEGLALLNGTDGMLGMLVMALADLRNLYTSADITAAALSLEALLGTDKVLAPELH	
HAL	187	PVELAEKEGLALVNGTDGMLGQLIMALADLDELDDIADATAAMSVEAQLGTDQVFRaelH	
		* * * * *	* * * * *
		* * * * *	* * * * *
STRG	246	A-IRPHPGQVSADNMSRVLAGSGLTGHHQDDAPRVQDAYSVRCAPQVNGAGRDTLDHAA	
HAL	247	EPLRPHPGQGRSAQNMFADSPIVASHREGDGRVQDAYSLRCSPOVTGAARDTIAHAR	
		* * * * *	* * * * *
		* * * * *	* * * * *
STRG	305	LVAGRELASSVDNPVPLPDGRVESNGNFHGAPVAYVLDFLAIVAADLGSICERRTRDLLD	
HAL	307	LVATRELAADNPVPLPSGEVTSNGNFHGAPVAYVLDFLAIAVADLGSIAERRTRMLD	
		* * * * *	* * * * *
		* * * * *	* * * * *

TEET40" 542E360

Figure 15, Cont'd.

STRG	365	KNRSHGLPPFLADDAGVDSGLMIAQYTQAALVSEMKRLAVPASADSI	PSSAMQEDHVS	MG
HAL	367	PARSRDLPAFLADDPGVDSGMMIAQYTQAGLVAENKRLAVPASVDSI	PSSAMQEDHVS	LG
		** ** *	** ** *	** ** *
STRG	425	WSAARKLRTAVDNLARIVAVELYAATRAIELRAAEGLT	PAPASEAVVAALRAAG	EGPGP
HAL	427	WHAARKLRTSVANLRRILAVEMLIAGRALDLRAP--	LKPGPATGAVLEVLRSKVA	-GPGQ
		* ** *	* ** *	* ** *
STRG	485	DRFLAPDLAAADTFVREGRLVA	AVE	
HAL	484	DRFLSAELEAAAYDLLANGSVH	KALE	
		***	* ** *	* ** *